

(FILE 'USPAT' ENTERED AT 12:11:21 ON 11 MAY 94)

L1 5233 S ?RELAXIN OR ?INSULIN OR ?INSULINLIKE OR IGF(W) (I OR II)
L2 433 S C(W) (CHAIN OR PEPTIDE)
L3 1265540 S MODIFI? OR ALTER? OR SHORTEN? OR TRUNCAT?
L4 126 S L1 AND L2
L5 110 S L3 AND L4
L6 45 S L2(P)L3

1. 5,304,473, Apr. 19, 1994, A-C-B proinsulin, method of manufacturing and using same, and intermediates in insulin production; Rama M. Belagaje, et al., 435/69.7, 252.33; 514/3; 530/303, 350; 536/23.51 [IMAGE AVAILABLE]

27. 4,639,333, Jan. 27, 1987, Process for converting preproinsulin analogs into insulins; Rainer Obermeier, et al., 530/303, 305; 930/10, 260 [IMAGE AVAILABLE]

01/10/94

> O <
OI IO IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : A-GeneSeq 13, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 1 Median 3 Standard Deviation 1.31
Times: CPU 00:00:24.10 Total Elapsed 00:01:29.00

Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4795

| Sequence Name | Description | Length | Score | Init. Opt. |
|----------------------------|--|--------|-------|------------|
| 1. R23998 | EGF/HB-EHM. | 208 | 8 | 8 |
| 2. P81758 | Sequence encoded by env gene | 735 | 8 | 8 |
| 3. R24126 | SIVmac239 env gene product. | 879 | 8 | 8 |
| 4. P80805 | Sequence of env protein of SI | 880 | 8 | 8 |
| 1. US-08-080-354B-3 (1-13) | **** 4 standard deviations above mean **** | | | |

R23998 EGF/HB-EHM.

ID R23998 standard; Protein; 208 AA.
AC R23998;

DT 09-NOV-1992 (first entry)

DE EGF/HB-EHM.

KW Heparin-binding epidermal growth factor; EGF; HB-EHM;

X 10 X
KRKPTGYGSRKKR

III I I III
90 X 100 X 110

LATPNKEHGKRRKKGGKGLGKRRDPCLRKYKDF

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 1.07
Times: CPU 00:01:09.13 Total Elapsed 00:04:16.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4792

| Sequence Name | Description | Length | Score | Init. Opt. |
|----------------------------|--|--------|-------|------------|
| 1. WMVETC | 8K protein - turnip crinkle v | 72 | 8 | 8 |
| 2. A37300 | heparin-binding EGF-like grow | 86 | 8 | 8 |
| 3. A38432 | heparin-binding EGF-like grow | 208 | 8 | 8 |
| 4. A41914 | diphtheria toxin receptor prec | 208 | 8 | 8 |
| 5. VCLJ52 | env polyprotein precursor - s | 880 | 8 | 8 |
| 6. S03068 | env protein - Human T-cell ly | 881 | 8 | 8 |
| 7. VCLJG3 | env polyprotein - simian immu | 881 | 8 | 8 |
| 8. VCLJG5 | env polyprotein - simian immu | 889 | 8 | 8 |
| 1. US-08-080-354B-3 (1-13) | **** 5 standard deviations above mean **** | | | |

WMVETC 8K protein - turnip crinkle virus

X 10 X
KRKPTGYGSRKKR

III I I III
20 30 40

NSLSDSDATGKRRKKGGKSAKRRKLVASHAASSV

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2

Mismatch penalty
Gap penalty

| | |
|--------------------------------|---------|
| Number of residues: | 4624329 |
| Number of sequences searched: | 37412 |
| Number of scores above cutoff: | 4751 |

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Times:
      CPU
      00:00:48.06
Total Elapsed
      00:02:50.00

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| Sequence Name | Description | Length | Score | Sig. | Frame |
|---------------|-------------|--------|-------|------|-------|
| Init. Opt. | | | | | |

| | | | |
|--------------------------|----|--------------------|----|
| Initial scores to save | 45 | Alignments to save | 15 |
| Optimized scores to save | 0 | Display context | 10 |

DT 04-AUG-1990 (first entry)

*
DE Amino acid sequence of open reading frame upstream of lysin gene on
DE fragment of lambda.gt10-lysin4
KW Bacteriophage phi-vML3; lambda .gt 10-lysin4.
X 10 X
DKKRTGYGSRRRK
II I I II
EFPSKKDEGTGYAFRKDGLYVGSIK
X 10 X 20

Results of the initial comparison of US-08-080-354B-6 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 1.07
Times: CPU 00:01:18.05 Total Elapsed 00:04:40.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4868

| Sequence Name | Description | Length | Score | Init. Opt. | Frame |
|--|--------------------------------|--------|-------|------------|--------|
| **** 4 standard deviations above mean **** | | | | | |
| 1. S08555 | ribosomal protein L15 - Halob | 29 | 7 | 7 | 4.69 0 |
| 2. S07769 | histone H2B.3, sperm - sea ur | 51 | 7 | 7 | 4.69 0 |
| 3. B32476 | hypothetical protein - mouse | 111 | 7 | 7 | 4.69 0 |
| 4. HSUR6P | histone H2B.2, sperm - sea ur | 143 | 7 | 7 | 4.69 0 |
| 5. HSURB2 | histone H2B.2, sperm - sea ur | 143 | 7 | 7 | 4.69 0 |
| 6. HSURB1 | histone H2B.2, sperm - sea ur | 144 | 7 | 7 | 4.69 0 |
| 7. HSUR8P | histone H2B.3, sperm - sea ur | 148 | 7 | 7 | 4.69 0 |
| 8. R5MXE | ribosomal protein L19.eR - Me | 149 | 7 | 7 | 4.69 0 |
| 9. D22735 | hypothetical nox3 protein - E | 334 | 7 | 7 | 4.69 0 |
| 10. S12190 | mobL protein - Thiobacillus f | 378 | 7 | 7 | 4.69 0 |
| 11. A44056 | nucleocapsid protein - canine | 382 | 7 | 7 | 4.69 0 |
| 12. S07824 | hypothetical protein 1 - fruit | 633 | 7 | 7 | 4.69 0 |
| 13. S14382 | hypothetical protein - fruit | 984 | 7 | 7 | 4.69 0 |
| **** 3 standard deviations above mean **** | | | | | |
| 14. S02786 | protamine 2a - horse (fragmen | 25 | 6 | 6 | 3.75 0 |
| 15. A34356 | protamine - Japanese quail | 57 | 6 | 6 | 3.75 0 |
| 16. S10754 | Protamine St2a - Horse | 62 | 6 | 6 | 3.75 0 |
| 17. A34326 | protamine - chicken | 62 | 6 | 7 | 3.75 0 |
| 18. S18671 | Heat shock protein 70 (Ssp1) | 65 | 6 | 6 | 3.75 0 |

19. GACH galline - chicken 65 6 7 3.75 0
20. A03316 homeotic protein Ac1 - Africa 67 6 6 3.75 0
21. JN0416 PabH protein - Rye 73 6 6 3.75 0
22. S01386 photosystem II phosphoprotein 73 6 6 3.75 0
23. S04148 photosystem II phosphoprotein 73 6 6 3.75 0
24. F2WTH photosystem II phosphoprotein 73 6 6 3.75 0
25. F2ZMBH photosystem II phosphoprotein 73 6 6 3.75 0
26. S04144 ribosomal protein S19 - Yersi 74 6 6 3.75 0
27. B41034 cytochrome-c oxidase chain VI 83 6 6 3.75 0
28. S06037 hypothetical protein - Serrat 84 6 6 3.75 0
29. S31482 sperm-specific protein Phi-1 92 6 6 3.75 0
30. R3EC19 ribosomal protein S19 - Esche 92 6 6 3.75 0
31. S08639 Homeotic protein zf-61 - Zebr 96 6 6 3.75 0
32. JC1195 plasminogen-related protein B 96 6 6 3.75 0
33. S03334 hypothetical protein 1 - Lact 97 6 6 3.75 0
34. S22454 REP protein - Wood tobacco (f 101 6 6 3.75 0
35. A43262 orf 2-hit - Bdellovibrio bact 101 6 6 3.75 0
36. PW0018 hypothetical protein 105 - Mi 105 6 6 3.75 0
37. PW0017 hypothetical protein 105 (grm 105 6 6 3.75 0
38. S19375 dihydroflavonol 4-reductase - 109 6 6 3.75 0
39. S34648 proteinase inhibitor precurs 114 6 6 3.75 0
40. S04158 adrenergic receptor beta-2 - 125 6 6 3.75 0
41. S31617 Protamine - Boll weevil 132 6 6 3.75 0
42. S10305 fau protein - Mouse 133 6 6 3.75 0
43. S21452 ubiquitin-like protein / ribo 133 6 6 3.75 0
44. S18101 ubiquitin-like protein / ribo 133 6 6 3.75 0
45. JC1278

1. US-08-080-354B-6 (1-13)

S08555 ribosomal protein L15 - Halobacterium cutirubrum

Initial Score = 7 Optimized Score = 7 Significance = 4.69
Residue Identity = 53% Matches = 7 Mismatches = 6
Gaps = 0 Conservative Substitutions

X 10 X

DKKRTGYGSRRRK

IIII III

TDKRRQGSRTTHGGGTHKNRGA

X 10 X 20

Results of the initial comparison of US-08-080-354B-6 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS
Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0
Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10
SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 0.94
Times: CPU 00:00:44.07 Total Elapsed 00:02:39.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4275

| Sequence Name | Description | Length | Score | Opt. |
|----------------|---------------------------------|--------|-------|------|
| 1. RL16_HALCU | 50S RIBOSOMAL PROTEIN HL16 (F | 29 | 7 | 7 |
| 2. H2B3_ECHES | HISTONE H2B.3, SPERM (FRAGMENT) | 40 | 7 | 7 |
| 3. H2B2_LVTPI | HISTONE H2B.2, SPERM. | 142 | 7 | 7 |
| 4. H2B2_STRPU | HISTONE H2B.2, SPERM. | 143 | 7 | 7 |
| 5. H2B2_PARAN | HISTONE H2B.2, SPERM. | 143 | 7 | 7 |
| 6. H2B3_METVA | HISTONE H2B.3, SPERM. | 148 | 7 | 7 |
| 7. MOBL_THIFE | PROBABLE 50S RIBOSOMAL PROTEIN | 149 | 7 | 7 |
| 8. MOBL_THIFE | MOBILIZATION PROTEIN MOBL. | 378 | 7 | 7 |
| 9. ZFPA_EPIVI | ZFPA PROTEIN (DEDB PROTEIN) (| 493 | 7 | 7 |
| 10. NOF1_DROME | 71 KD PROTEIN IN NOF-FB TRANS | 633 | 7 | 7 |
| 11. NOF_DROME | 112 KD PROTEIN IN NOF-FB TRANS | 984 | 7 | 7 |
| 12. SWH1_YEAST | SWH1 PROTEIN. | 1141 | 7 | 7 |

1. US-08-080-354B-6 (1-13)
RL16_HALCU 50S RIBOSOMAL PROTEIN HL16 (FRAGMENT). DE 50S RIBOSOMAL
PROTEIN HL16 (FRAGMENT).
OS HALOBACTERIUM CUTIRUBRUM.

X 10 X
DKKRTGYGSRRRK
|||||
TDKRRQRGSRTHGGGTHKNRGA

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : A-GeneSeq 13, all entries
PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05

Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 1 Median 3 Standard Deviation 1.31

Times: CPU 00:00:23.03 Total Elapsed 00:01:31.00

Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4673

| Sequence Name | Description | Length | Score | Opt. |
|---------------|---------------------------------|--------|-------|------|
| 1. R22590 | Nonlinear peptide 8deltaTNF(1 | 22 | 7 | 7 |
| 2. R13070 | SIV500 fusion protein. | 12 | 6 | 6 |
| 3. R03460 | Intracellular retention motif | 48 | 6 | 6 |
| 4. R04933 | Interferon-gamma receptor seg | 223 | 6 | 6 |
| 5. P60518 | Sequence of bovine inhibin B | 288 | 6 | 6 |
| 6. R34544 | Tet e gene product from pMW10 | 314 | 6 | 6 |
| 7. R37873 | Tet e gene product from pMW10 | 314 | 6 | 6 |
| 8. R29623 | Tet e gene product from pMW10 | 314 | 6 | 6 |
| 9. R20991 | Protein "d" encoded by mycobact | 354 | 6 | 6 |
| 10. R25853 | MSH-dependent protein obtd. f | 389 | 6 | 6 |
| 11. R32108 | Pectin esterase | 389 | 6 | 6 |
| 12. P80300 | Pectin esterase. | 389 | 6 | 6 |
| 13. R32020 | Sequence of a eukaryotic tran | 414 | 6 | 6 |
| 14. R28956 | HIV gp160-MN precursor up to | 513 | 6 | 6 |
| 15. P61363 | Soybean glycinin A5A4B3 subun | 561 | 6 | 6 |
| 16. R34938 | Human glucose regulated prote | 656 | 6 | 6 |
| 17. R81758 | Sequence encoded by env gene | 735 | 6 | 6 |
| 18. R13786 | HIV multifunctional fusion po | 770 | 6 | 6 |
| 19. R14903 | HIV-1(MN) env protein. | 856 | 6 | 6 |
| 20. R14904 | HIV-1(MN-ST1) env protein. | 857 | 6 | 6 |
| 21. R24126 | SIVmac239 env gene product. | 879 | 6 | 6 |
| 22. P80805 | Sequence of env protein of SI | 880 | 6 | 6 |
| 23. R10333 | Deduced sequence of tomato ni | 911 | 6 | 6 |
| 24. R20027 | C-terminal amidation enzyme. | 953 | 6 | 6 |
| 25. R11113 | Equine C-terminal amidating e | 980 | 6 | 6 |
| 26. R20025 | C-terminal amidation enzyme. | 1020 | 6 | 6 |
| 27. R3547 | Sequence of the alpha 1C huma | 1967 | 6 | 6 |
| 28. R35081 | ZYMV polyprotein. | 3080 | 6 | 6 |
| 29. P81769 | Sequence encoded by top readi | 3211 | 6 | 6 |
| 30. R37619 | Sequence of the C-chain/A-cha | 7 | 5 | 5 |
| 31. R29298 | Nerve growth stimulating prot | 9 | 5 | 5 |
| 32. R36857 | Insulin-like growth factor-I | 10 | 5 | 5 |
| 33. R37513 | 30Arg, 32Tyr 22-32 Peptide C | 11 | 5 | 5 |
| 34. R36911 | Insulin-like growth factor-II | 12 | 5 | 5 |
| 35. R12491 | Lys(342)-alpa-1-antitrypsin d | 12 | 5 | 5 |
| 36. P80993 | Sequence of unique protease y | 13 | 5 | 5 |
| 37. R36856 | Insulin-like growth factor-I | 14 | 5 | 5 |
| 38. R26100 | Proposed Superantigen binding | 15 | 5 | 5 |
| 39. R10929 | Relaxin C peptide epitope II. | 15 | 5 | 5 |
| 40. R36852 | Insulin-like growth factor-I | 18 | 5 | 5 |
| 41. R36848 | Insulin-like growth factor-I | 18 | 5 | 5 |
| 42. R28791 | High endotoxin affinity polyp | 18 | 5 | 5 |
| 43. R28790 | High endotoxin affinity polyp | 18 | 5 | 5 |
| 44. R28787 | High endotoxin affinity polyp | 18 | 5 | 5 |
| 45. R28783 | High endotoxin affinity polyp | 18 | 5 | 5 |

1. US-08-080-354B-7 (1-13)

R22590 Nonlinear peptide 8deltaTNF(144-157). KW Tumour necrosis
factor; TNFalpha; polylysine.
OS Synthetic.

X 10 X
DKKRTGYGSRKKR

|||
DYLAGFKAHGKRYGGGRKKG
10 20 X

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 2 3 1.09
Times: CPU Total Elapsed
 00:01:14.01 00:03:57.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4955

| Sequence Name | Description | Length | Score | Opt. | Frame |
|---------------|-------------------------------|--------|-------|------|-------|
| 1. D22735 | hypothetical nox3 protein - E | 334 | 9 | 6.42 | 0 |
| 2. JC1409 | heparin-binding EGF-like grow | 208 | 8 | 5.50 | 0 |
| 3. S08555 | ribosomal protein L15 - Halob | 29 | 7 | 4.58 | 0 |
| 4. S16512 | Hypothetical protein - Yeast | 182 | 7 | 4.58 | 0 |
| 5. JC1410 | heparin-binding EGF-like grow | 208 | 7 | 4.58 | 0 |
| 6. S33114 | DIOR COP protein - variola vi | 248 | 7 | 4.58 | 0 |
| 7. G36847 | FIOR protein - variola virus | 248 | 7 | 4.58 | 0 |
| 8. S29871 | DNA-(apurinic or apyrimidinic | 367 | 7 | 4.58 | 0 |
| 9. A28940 | secY protein - Mycoplasma cap | 482 | 7 | 4.58 | 0 |
| 10. B43827 | cytochrome d complex terminal | 523 | 7 | 4.58 | 0 |
| 11. A36705 | heat shock protein groEL - Br | 544 | 7 | 4.58 | 0 |
| 12. A36705 | transcriptional activator fhl | 686 | 7 | 4.58 | 0 |
| 13. S12079 | fhlA protein - Escherichia co | 692 | 7 | 4.58 | 0 |
| 14. A25064 | regulatory protein ARGRII - y | 880 | 7 | 4.58 | 0 |
| 15. A41667 | nitrate reductase (NADH) - wi | 918 | 7 | 4.58 | 0 |
| 16. VCLJCC | env polyprotein precursor - c | 966 | 7 | 4.58 | 0 |

1. US-08-080-354B-7 (1-13)

D22735 hypothetical nox3 protein - Emericella nidulans
Initial Score = 9 Optimized Score = 6.42
Residue Identity = 69% Matches = 9 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

X 10 X
DKKRTGYGSRKKR

||||| |||

HSLDVSLAYIYIKRLGYSVKVKKKNNAFLIV

110 X 120 X 130

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 2 3 0.97
Times: CPU Total Elapsed
 00:00:44.00 00:02:35.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4341

| Sequence Name | Description | Length | Score | Opt. | Frame |
|----------------|-------------------------------|--------|-------|------|-------|
| 1. RL16 HALCU | 50S RIBOSOMAL PROTEIN HL16 (F | 29 | 7 | 5.14 | 0 |
| 2. RL34_BORBU | 50S RIBOSOMAL PROTEIN L34. | 51 | 7 | 5.14 | 0 |
| 3. TPM_HANPO | TROPOMYOSIN-LIKE PROTEIN (FRA | 182 | 7 | 5.14 | 0 |
| 4. VD10_VARV | PROTEIN D10. | 248 | 7 | 5.14 | 0 |
| 5. APNI_YEAST | DNA-(APURINIC OR APYRIMIDINIC | 361 | 7 | 5.14 | 0 |
| 6. SECY_MYCCA | PREPROTEIN TRANSLOCASE SECY S | 482 | 7 | 5.14 | 0 |
| 7. CYDA_ECOLI | CYTOCHROME D UBIQUINOL OXIDAS | 522 | 7 | 5.14 | 0 |
| 8. FHIA_ECOLI | FORMATE HYDROGENLYASE TRANSCR | 692 | 7 | 5.14 | 0 |
| 9. ENV_HV128 | ENVELOPE POLYPROTEIN GP160 PR | 863 | 7 | 5.14 | 0 |
| 10. ARG2_YEAST | ARGININE METABOLISM REGULATIO | 880 | 7 | 5.14 | 0 |
| 11. NIA_CUCVA | NITRATE REDUCTASE (EC 1.6.6.1 | 918 | 7 | 5.14 | 0 |
| 12. ENV_CAEVC | ENV POLYPROTEIN PRECURSOR (CO | 966 | 7 | 5.14 | 0 |

1. US-08-080-354B-7 (1-13)

RL16 HALCU 50S RIBOSOMAL PROTEIN HL16 (FRAGMENT). DE 50S RIBOSOMAL
PROTEIN HL16 (FRAGMENT).
OS HALOBACTERIUM CUTIRUBRUM.
X 10 X

DKKRTGYGSRKKR

||||| |||

TDKRRQRGSRTHGGGTHKNSRGA

X 10 X 20

Results of the initial comparison of US-08-080-354B-8 (1-13) with:
Data bank : A-GeneSeq 13, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05

Cutoff score 0

Randomization group 0

1. US-08-080-354B-8 (1-13)

R36857 Insulin-like growth factor-I functional derivative

X 10 X

KRPITYGSGRRRK
IIIIII I
KPIYGGSSSR

X 10

Times: CPU Total Elapsed
 00:00:24.10 00:01:35.00

Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4840

CC The sequence is that of a functional derivative of human insulin-like growth factor (IGF)-I which promotes the survival of retinal neuronal cells. It can be used for the treatment of retinal neuronal tissues which are suffering from the effects of injury, ageing and/or disease such as photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration, ischemic neuronal degeneration, inherited retinal dystrophy, diabetic retinopathy, Alzheimer's disease, infantile CC malignant osteopetrosis, ceroid lipofuscosiis or cholestasis. CC Results of the initial comparison of US-08-080-354B-8 (1-13) with: Data bank : PIR 38, all entries

Sequence Name Description Length Score Init. Opt. Sig. Frame

1. R36857 Insulin-like growth factor-I 10 7 8 4.55 0
2. R36911 Insulin-like growth factor-II 12 7 8 4.55 0
3. R36852 Insulin-like growth factor-I 18 7 8 4.55 0
4. R36848 Insulin-like growth factor-I 18 7 8 4.55 0
5. P50378 Antigenic peptide fragment of 18 7 8 4.55 0
6. R36910 Insulin-like growth factor-II 20 7 8 4.55 0
7. P40341 IGF-I (26-46). 21 7 8 4.55 0
8. R13324 Cd peptide used in protective 29 7 8 4.55 0
9. P81209 C-domain of IGF-1 (Fra-B-7). 30 7 8 4.55 0
10. P60079 Sequence encoded by peptide C 31 7 8 4.55 0
11. P80431 Sequence of N-terminal portio 35 7 8 4.55 0
12. P90515 Derivative of insulin-like gr 62 7 8 4.55 0
13. P91501 New insulin-like growth facto 62 7 8 4.55 0
14. R36847 Insulin-like growth factor-I 67 7 8 4.55 0
15. R36846 Insulin-like growth factor-I. 70 7 8 4.55 0
 IFG-I. 70 7 8 4.55 0
 Sequence of human insulin-lik 70 7 8 4.55 0
16. P40034 Modified mammalian somatomedi 70 7 8 4.55 0
17. R10587 Modified mammalian somatomedi 70 7 8 4.55 0
18. R10586 Sequence of human insulin-lik 70 7 8 4.55 0
19. P71539 Sequence of oxidative human i 70 7 8 4.55 0
20. P70414 Human insulin-like growth fac 70 7 8 4.55 0
21. R06306 Human insulin-like growth fac 70 7 8 4.55 0
22. R06307 Human insulin-like growth fac 70 7 8 4.55 0
23. R06307 Analogue IGF252 of human insu 70 7 8 4.55 0
24. P94660 Analogue IGF130 of human insu 70 7 8 4.55 0
25. P94661 Analogue IGF122 of human insu 70 7 8 4.55 0
26. P93366 New insulin-like growth facto 70 7 8 4.55 0
27. P91502 Insulin-like Growth Factor-I. 71 7 8 4.55 0
28. R21709 Synthetic human insulin-like 71 7 8 4.55 0
29. P50872 59-Val insulin-like growth fa 71 7 8 4.55 0
30. P50098 Methionine-insulin-like growt 71 7 8 4.55 0
31. P81221 Synthetic human insulin growt 71 7 8 4.55 0
32. R05281 Amino acid sequence of Insuli 71 7 8 4.55 0
33. R05281 Analogue IGF132 of human insu 71 7 8 4.55 0
34. P94729 Lys-gal/IGF-1 fusion protein 72 7 8 4.55 0
35. R11422 Beta-gal/IGF-1 fusion protein 74 7 8 4.55 0
36. R13759 Beta-gal IGF-1 fusion protein 76 7 8 4.55 0
37. R13758 Insulin-like growth factor-I 78 7 8 4.55 0
38. P81213 Fusion protein of insulin-lik 89 7 8 4.55 0
39. P40026 Short fusion protein contg. i 90 7 8 4.55 0
40. P40024 Sequence of insulin growth fa 95 7 8 4.55 0
41. R37549

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 1.08

Times: CPU 00:01:15.05 Total Elapsed 00:04:07.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4776

Sequence Name Description Length Score Init. Opt. Sig. Frame

1. S12843 *** 5 standard deviations above mean **** 137 8 5.56 0
 core antigen - duck hepatitis 137 8 5.56 0
2. NKVLHH core antigen - heron hepatitis 305 8 5.56 0

3. NKVLDS core antigen - duck hepatitis 305 8
4. NKVLMD core antigen - duck hepatitis 305 8
5. NKVLBD core antigen - duck hepatitis 305 8
6. NKVLID core antigen - duck hepatitis 305 8
*** 4 standard deviations above mean ***
7. S07198 Insulin-like growth factor - 70 7
8. A37415 Insulin-like growth factor I 70 7
9. A32857 Insulin-like growth factor I 70 7
10. S00465 Insulin-like growth factor I 70 7
11. IG801 Insulin-like growth factor I 70 7
12. A28504 Insulin-like growth factor I 108 7
13. JQ1941 hypothetical 12.8K protein - 116 7
14. A35766 platelet factor 4, interferon 126 7
15. A27849 Insulin-like growth factor IA 127 7
16. JH0133 Insulin-like growth factor I 127 7
17. A25540 Insulin-like growth factor IA 127 7
18. B40912 Insulin-like growth factor I 127 7
19. B25540 Insulin-like growth factor IB 133 7
20. A40912 Insulin-like growth factor I 133 7
21. A34938 Insulin-like growth factor IA 134 7
22. JN0088 Insulin-like growth factor I 137 7
23. A35552 Insulin-like growth factor Ia 137 7
24. IG651 Insulin-like growth factor I 137 7
25. S22878 Insulin-like growth factor-I 138 7
26. B33390 Insulin-like growth factor I 138 7
27. S12672 Insulin-like growth factor pr 153 7
28. S12825 Insulin-like growth factor I 153 7
29. S30519 IGF-1a - Human 153 7
30. A41399 Insulin-like growth factor IA 153 7
31. A36079 Insulin-like growth factor I 153 7
32. B27804 Insulin-like growth factor IA 153 7
33. IGHUI Insulin-like growth factor IA 153 7
34. S22877 Insulin-like growth factor-I 154 7
35. A33390 Insulin-like growth factor I 154 7
36. A26859 Insulin-like growth factor IB 159 7
37. A27804 Insulin-like growth factor I 181 7
38. S30540 IGF-1b - Human 195 7
39. A26181 Insulin-like growth factor IB 195 7
40. IGHUIB Insulin-like growth factor IB 195 7
41. JH0550 histone H1t - human 207 7
42. S08031 nucleocapsid protein - human 389 7
43. S15715 chorismate synthase - pink co 447 7
44. A41197 chorismate synthase - pink co 447 7
45. S18153 Serotonin receptor 5HT-dro2A 834 7

1. US-08-080-354B-8 (1-13)

S12843 core antigen - duck hepatitis virus (fragment)

X 10 X

KRKPTGYGSRRRK

|||||

AQGGRKTTTGTRKPRGLPEPRRRKVKTTVTGRR
80 90 X 100

7. US-08-080-354B-8 (1-13)

S07198 Insulin-like growth factor - Sheep

X 10 X

KRKPTGYGSRRRK

|||||

QFVCGDRGFYENKPTGYGSSRRRAPQTGIVDEC
20 X 30 X 40

Results of the initial comparison of US-08-080-354B-8 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

| | | | |
|---------------------|---------|-----------------|----|
| Similarity matrix | Unitary | K-tuple | 2 |
| Mismatch penalty | 1 | Joining penalty | 20 |
| Gap penalty | 1.00 | Window size | 13 |
| Gap size penalty | 0.05 | | |
| Cutoff score | 0 | | |
| Randomization group | 0 | | |

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

| | | | |
|---------|------|--------|--------------------|
| Scores: | Mean | Median | Standard Deviation |
| | 2 | 3 | 0.96 |

Times: CPU 00:00:48.03 Total Elapsed 00:02:47.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4163

| Sequence Name | Description | Length | Score | Init. Opt. |
|----------------|-------------------------------|--------|-------|------------|
| 1. CORA_HPBHE | CORE ANTIGEN. | 305 | 8 | 8 6.27 0 |
| 2. CORA_HPBDM | CORE ANTIGEN. | 305 | 8 | 8 6.27 0 |
| 3. CORA_HPBDU | CORE ANTIGEN. | 305 | 8 | 8 6.27 0 |
| 4. CORA_HPBDC | CORE ANTIGEN. | 305 | 8 | 8 6.27 0 |
| 5. CORA_HPBDB | CORE ANTIGEN. | 305 | 8 | 8 6.27 0 |
| 6. H2BN_STRPU | LATE HISTONE H2B.L3. | 122 | 7 | 7 5.22 0 |
| 7. MIG_MOUSE | GAMMA INTERFERON INDUCED MONO | 126 | 7 | 7 5.22 0 |
| 8. IGFI_MOUSE | INSULIN-LIKE GROWTH FACTOR IA | 127 | 7 | 8 5.22 0 |
| 9. IGFI_CAVPO | INSULIN-LIKE GROWTH FACTOR I | 130 | 7 | 8 5.22 0 |
| 10. IGFB_MOUSE | INSULIN-LIKE GROWTH FACTOR IB | 133 | 7 | 8 5.22 0 |
| 11. IGFA_RAT | INSULIN-LIKE GROWTH FACTOR IA | 153 | 7 | 8 5.22 0 |
| 12. IGFA_HUMAN | INSULIN-LIKE GROWTH FACTOR IA | 153 | 7 | 8 5.22 0 |
| 13. IGFI_XENLA | INSULIN-LIKE GROWTH FACTOR I | 153 | 7 | 8 5.22 0 |
| 14. IGFI_PIG | INSULIN-LIKE GROWTH FACTOR I | 153 | 7 | 8 5.22 0 |
| 15. IGFI_CHICK | INSULIN-LIKE GROWTH FACTOR I | 153 | 7 | 8 5.22 0 |
| 16. IGFI_SHEEP | INSULIN-LIKE GROWTH FACTOR I | 154 | 7 | 8 5.22 0 |
| 17. IGFI_BOVIN | INSULIN-LIKE GROWTH FACTOR I | 154 | 7 | 8 5.22 0 |
| 18. IGFB_RAT | INSULIN-LIKE GROWTH FACTOR IB | 181 | 7 | 8 5.22 0 |
| 19. IGFB_HUMAN | INSULIN-LIKE GROWTH FACTOR IB | 195 | 7 | 8 5.22 0 |
| 20. H1T_HUMAN | HISTONE H1T. | 206 | 7 | 7 5.22 0 |
| 21. AROC_CORSE | CHORISMATE SYNTHASE PRECURSOR | 447 | 7 | 7 5.22 0 |
| 22. SHTA_DROME | 5-HYDROXYTRYPTAMINE RECEPTOR | 834 | 7 | 7 5.22 0 |
| 23. EBN6_EBV | EBNA-6 NUCLEAR PROTEIN (EBNA- | 992 | 7 | 7 5.22 0 |

1. US-08-080-354B-8 (1-13)

CORA_HPBHE CORE ANTIGEN.

OS HERON HEPATITIS B VIRUS.

OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HEPADNAVIRIDAE.

10 X

• . . : •
KRKPTGYGSRRRK

||| | |||

AQGRNQTKGTRKPRGLEPRRRKVKTTVVYGR
240 250 260 270